



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/820,425A  
Source: OIPE  
Date Processed by STIC: 08/08/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/20, 925A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length  
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)  
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)  
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☒ Use of n's or Xaa's  
(NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

DATE: 08/08/2001

PATENT APPLICATION: US/09/820,425A

TIME: 10:50:21

Input Set : A:\Dex-2031.app

Output Set: N:\CRF3\08082001\I820425A.raw

**Does Not Comply  
Corrected Diskette Needed**

```

3 <110> APPLICANT: Chen, Sei-Yu
4     Hu, Ping
5     Recipon, Herve
6     Macina, Roberto
8 <120> TITLE OF INVENTION: Compositions and Methods of Diagnosing, Monitoring,
9     Staging, Imaging and Treating Lung Cancer
11 <130> FILE REFERENCE: DEX-0203
13 <140> CURRENT APPLICATION NUMBER: US/09/820,425A
14 <141> CURRENT FILING DATE: 2001-03-29
16 <150> PRIOR APPLICATION NUMBER: 60/192,921
17 <151> PRIOR FILING DATE: 2000-03-29
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 132
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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30 gcaggttccc ataagtagag taacatcttt ctcttgaaat aggtgctgtg tcaaagtctg 120
31 tatcataagc tt                                     132
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 118
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <400> SEQUENCE: 2
40 accacccttc cagcagcagc tgtgccttgg cacaatgcat tcagcatctg cagagaactg 60
41 gacatggctg gagacttggg gttccataac aatgcctgga acatgatgca gcaagctt 118
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 107
46 <212> TYPE: DNA
47 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 3
50 gaacggatca gcataacttt gggataaaat tagccgacag tttgtggact ctccagcatg 60
51 cgcctgtttg ctcggtgctg ttctctcgat aaatcacaac aaagctt 107
54 <210> SEQ ID NO: 4
55 <211> LENGTH: 137
56 <212> TYPE: DNA
57 <213> ORGANISM: Homo sapiens
59 <400> SEQUENCE: 4
60 actgttctctg ttggccgagt ggagactggt gttcatcaaa accctgtgta tggttgggtca 60
61 cgcatttgcg tccagatcga actgttacag acgtgaaggt aagaatcgtg tctgaaagtg 120
62 cacctatgac agctttg                                     137
65 <210> SEQ ID NO: 5
66 <211> LENGTH: 101
67 <212> TYPE: DNA
68 <213> ORGANISM: Homo sapiens

```

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Input Set : A:\Dex-2031.app

Output Set: N:\CRF3\08082001\I820425A.raw

70 &lt;400&gt; SEQUENCE: 5

71 taccagtgct tggtagacaag ctggtgtact caaggggtcat agcgggttgta ctgagagaag 60  
 72 atcgtagtc cgtcacgaa ttccacacga agatacgagg c 101

75 &lt;210&gt; SEQ ID NO: 6

76 &lt;211&gt; LENGTH: 704

77 &lt;212&gt; TYPE: DNA

78 &lt;213&gt; ORGANISM: Homo sapiens

80 &lt;400&gt; SEQUENCE: 6

81 acacatggag accatgatgc gaacggggac tgccagtgga tatgagggct tttatgaaag 60  
 82 ggagtttgct ctgatgtgtg tgtttccgct cccaaaacac acacacagca gcacacagtc 120  
 83 gcgatacatc atatttcaat ccgttgcta gctcagatct ctgtggttat ggggtaacaa 180  
 84 acagtcggat gcagaaaaac tatccatgaa ttcagcaaac acagttagcc gtaggtcgaa 240  
 85 gaatccctaa accgctctta acaatcatat aatccatact gctgagcgac attagactgg 300  
 86 gctgctacac ctgctcctgt tcagccgaca gcccagcca tgtacccccg catcctcctt 360  
 87 ctccataatat ctcccacaag acgatcaca gctatggcca gtacatcagt ggctcaatag 420  
 88 cctgacatcc ctgctgctgc caactcgta ctcccgcctc acacagttcc accacaacca 480  
 89 taccgagcca acccgccccc accagccccc caccgcccga gggccgcgcc ccacgcccga 540  
 90 ccccacggcc acccccaccg accgagccac cccccccccc cgtcccacac ccgaccaggc 600  
 91 cccccccacc ccccacgac cgcaaccaga gccccaccg ccgcaccgcc ccccgccccg 660  
 92 ccgcccagca ccccaccgcg aaccaccgcc cccccccccc gcac 704

95 &lt;210&gt; SEQ ID NO: 7

96 &lt;211&gt; LENGTH: 145

97 &lt;212&gt; TYPE: DNA

98 &lt;213&gt; ORGANISM: Homo sapiens

100 &lt;220&gt; FEATURE:

101 &lt;221&gt; NAME/KEY: unsure

102 &lt;222&gt; LOCATION: (101)

104 &lt;220&gt; FEATURE:

105 &lt;221&gt; NAME/KEY: unsure

106 &lt;222&gt; LOCATION: (125)..(126)

108 &lt;400&gt; SEQUENCE: 7

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 W--> 110 cagtgttga gagttgagag cgagactcgt gtgtggttac nagacttcta cagtgtcaac 120  
 W--> 111 atgchicagc agaaaataag tcttg 145

114 &lt;210&gt; SEQ ID NO: 8

115 &lt;211&gt; LENGTH: 715

116 &lt;212&gt; TYPE: DNA

117 &lt;213&gt; ORGANISM: Homo sapiens

119 &lt;400&gt; SEQUENCE: 8

120 accatggtaa gaaacagttt taacagtaga tcacgtatca gattgaatga taataaatca 60  
 121 atttgggaaa tgagttagat tctggacagt ctgatacgt gatctactag ctcaacaact 120  
 122 gtatcattac cactggtaca gtataagatc tcaactaacg ccgcaaaccg acatttcaga 180  
 123 ctatctaacc attacatttg tacaattcca tagtgagtat caacgtttat cactacaccg 240  
 124 aagtgcatta agcacacatg cagtgcacaa cattctacaa actgcagcac caccatggcg 300  
 125 tctacggcga attcagctag cgggctgata tcacagacac gaccactagc cccactcgc 360  
 126 ttatcactac tatacaccta tatacgtgct tgaactaaca ctatcttcga tagtttaact 420  
 127 cgtacctttt gctcgcacac ctacacaggac acagttcgtc catacaccta gacccctcg 480  
 128 ggccacggcg cctgcacccc cggcatacgg acaaccgcca ctactcgc cccggaccct 540  
 129 aacagcacga cgcccaccta ccatgactcc caccaaccca acctgtcgac aacgacaagg 600

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Input Set : A:\Dex-2031.app

Output Set: N:\CRF3\08082001\I820425A.raw

130 acgcaacact acaacaagca aaataccact ggccaccgca tagcgccgcc acacacacat 660  
131 ggcacagcag gacagctacc cctgctgcc cacaactggac catcccgct ccaca 715  
134 <210> SEQ ID NO: 9  
135 <211> LENGTH: 370  
136 <212> TYPE: DNA  
137 <213> ORGANISM: Homo sapiens  
139 <220> FEATURE:  
140 <221> NAME/KEY: unsure  
141 <222> LOCATION: (92)..(93)  
143 <220> FEATURE:  
144 <221> NAME/KEY: unsure  
145 <222> LOCATION: (205)..(206)  
147 <220> FEATURE:  
148 <221> NAME/KEY: unsure  
149 <222> LOCATION: (225)..(226)  
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152 <221> NAME/KEY: unsure  
153 <222> LOCATION: (243)..(244)  
155 <220> FEATURE:  
156 <221> NAME/KEY: unsure  
157 <222> LOCATION: (268)  
159 <220> FEATURE:  
160 <221> NAME/KEY: unsure  
161 <222> LOCATION: (285)  
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164 <221> NAME/KEY: unsure  
165 <222> LOCATION: (297)..(298)  
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168 <221> NAME/KEY: unsure  
169 <222> LOCATION: (308)  
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173 <222> LOCATION: (311)  
175 <220> FEATURE:  
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181 <222> LOCATION: (322)  
183 <220> FEATURE:  
184 <221> NAME/KEY: unsure  
185 <222> LOCATION: (327)  
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189 <222> LOCATION: (349)  
191 <220> FEATURE:  
192 <221> NAME/KEY: unsure  
193 <222> LOCATION: (355)  
195 <220> FEATURE:

*requires build 223  
for description of "*

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Input Set : A:\Dex-2031.app

Output Set: N:\CRF3\08082001\I820425A.raw

196 <221> NAME/KEY: unsure  
 197 <222> LOCATION: (357)  
 199 <220> FEATURE:  
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 201 <222> LOCATION: (359)  
 203 <220> FEATURE:  
 204 <221> NAME/KEY: unsure  
 205 <222> LOCATION: (361)  
 207 <220> FEATURE:  
 208 <221> NAME/KEY: unsure  
 209 <222> LOCATION: (370)  
 211 <220> FEATURE:  
 212 <221> NAME/KEY: unsure  
 213 <222> LOCATION: (334) ✓  
 215 <220> FEATURE:  
 216 <221> NAME/KEY: unsure  
 217 <222> LOCATION: (336) ✓  
 219 <220> FEATURE:  
 220 <221> NAME/KEY: unsure  
 221 <222> LOCATION: (341) ✓  
 223 <400> SEQUENCE: 9  
 224 atgagggcca gcagcttctt gatcgtggtg gtttctctca tcgctgggat gctggttcta 60  
 W--> 225 gaaggcagcg tgtcacgctg gaatgttctt gnttaaatg tgttcaatga aacctctgca 120  
 226 aagtgcgcgt gttccaattc aatgtgagca agatccctgt taaagatgac aatgtttcag 180  
 W--> 227 ttaacaggtc agagataaca gtcannhaagc gcaagagcca tgtcnnaaag tgtccatgtc 240  
 W--> 228 tcnncacata agacctggtc gtctctgngc cccaaatata tactttggaa ttccggnttt 300  
 W--> 229 ggcggccantg nttttgaant tccccctt taanctggc nttggcttnt tggahamag 360  
 W--> 230 naattaactn 370  
 233 <210> SEQ ID NO: 10  
 234 <211> LENGTH: 181  
 235 <212> TYPE: DNA  
 236 <213> ORGANISM: Homo sapiens  
 238 <220> FEATURE:  
 239 <221> NAME/KEY: unsure  
 240 <222> LOCATION: (74)  
 242 <220> FEATURE:  
 243 <221> NAME/KEY: unsure  
 244 <222> LOCATION: (98)  
 246 <220> FEATURE:  
 247 <221> NAME/KEY: unsure  
 248 <222> LOCATION: (140)  
 250 <220> FEATURE:  
 251 <221> NAME/KEY: unsure  
 252 <222> LOCATION: (173)  
 254 <400> SEQUENCE: 10  
 255 acataataga acttatttat ggagttagaa attttagtg ttatccagga ttgattttca 60  
 W--> 256 ctttgatcac atcttcacag ataataaat attttcahag ttttttttct tattaacag 120  
 W--> 257 ctctggtgca tagttttttt tttctgggtt atagccttct atcccaaata tanaagctgt 180  
 258 g 181

*requires field 223 for description of n.*  
*394 396 398 OK*  
*requires field 223 for description of n.*  
*requires*

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Input Set : A:\Dex-2031.app

Output Set: N:\CRF3\08082001\I820425A.raw

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261 <210> SEQ ID NO: 11
262 <211> LENGTH: 124
263 <212> TYPE: DNA
264 <213> ORGANISM: Homo sapiens
266 <400> SEQUENCE: 11
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268 gattctagag tgtatgtcac cactgtagat atacaactca tcacagcaca cattccaaga 120
269 ctct 124
272 <210> SEQ ID NO: 12
273 <211> LENGTH: 311
274 <212> TYPE: DNA
275 <213> ORGANISM: Homo sapiens
277 <400> SEQUENCE: 12
278 actccagctc tgtgtgcaag gagatgtgct ggaatgtcac agcatcgtat agcaaagagc 60
279 atattggcaa cagcttggat ggccagcaga aggagcccaa atgtgtgatt catattcact 120
280 agtcgaataa ttgaatacta caatatacac catatatact agactgtatg tgttgttcta 180
281 tactatagtg attgacttga actccattca gtgaaaaaaa tggaagaatt agctatttgt 240
282 atccatatgg gatacaaaaa agcagggtaa caaagaatc tacatcatct tgccatttgc 300
283 aggtaaagct t 311
286 <210> SEQ ID NO: 13
287 <211> LENGTH: 22
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence ✓
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic ✓
294 <400> SEQUENCE: 13
295 cgagtggaga ctggtgttca tc 22
298 <210> SEQ ID NO: 14
299 <211> LENGTH: 24
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence ✓
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic ✓
306 <400> SEQUENCE: 14
307 gcactttcag acacgattct tacc 24
310 <210> SEQ ID NO: 15
311 <211> LENGTH: 26
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
318 <400> SEQUENCE: 15
319 ggtgagaata caacagaagt ccaact 26
322 <210> SEQ ID NO: 16
323 <211> LENGTH: 23
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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## VERIFICATION SUMMARY

DATE: 08/08/2001

PATENT APPLICATION: US/09/820,425A

TIME: 10:50:22

Input Set : A:\Dex-2031.app

Output Set: N:\CRF3\08082001\I820425A.raw

L:110 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:111 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:225 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:227 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:228 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:229 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:230 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:256 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10  
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:257 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10  
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10